<u>**IN THE CLAIMS:**</u>

Please amend claims 1-12, add new claims 13-15 as follows:

1.   (Currently Amended) A method for assembling nucleic acid base sequences comprising the steps of:

<u>providing a plurality of nucleic acid base sequences;</u>

moving a window of <u>a</u> fixed length along a first nucleic acid base sequence <u>of the plurality of nucleic acid base sequences to define a first fixed-length partial sequence</u> and simultaneously searching for a second nucleic acid base sequence <u>among the plurality of nucleic acid base sequences</u> which has a <u>second fixed-length</u> partial sequence at a terminal region thereof <u>exactly</u> matching with <u>the first fixed-length partial</u> sequence defined by the window;

determining whether the second nucleic acid base sequence searched in said <u>moving</u> step and the first nucleic acid base sequence can be assembled or not <u>by comparing a sequence adjacent to said first fixed-length partial sequence of said first nucleic acid base sequence with a sequence adjacent to said second fixed-length partial sequence of the second nucleic acid base sequence to be sufficiently similar via a greedy alignment algorithm</u>; and

assembling said first nucleic acid base sequence and said second nucleic acid bases sequence if ~~said step determines that~~ the second nucleic acid base sequence and the first nucleic acid base sequence ~~can~~ <u>are determined to</u> be assembled.

2.   (Currently Amended) A method for assembling nucleic acid base sequences <u>according to claim 1,</u> ~~comprising the steps of:~~

~~moving a window of fixed length along a first nucleic acid base sequence and simultaneously searching for a second nucleic acid base sequence which has a partial sequence at a terminal region thereof matching with a sequence defined by the window;~~

~~determining whether the second nucleic acid base sequence searched in said step and the first nucleic acid base sequence can be assembled or not; and~~

~~assembling said first nucleic acid base sequence and said second nucleic acid base sequence if said step determines that the second nucleic acid base sequence and the first~~

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nucleic acid base sequence can be assembled,

wherein the nucleic acid base sequence assembled in said assembling step is used as a [[new]] **reconstructed** first nucleic acid base sequence to repeatedly carry out said moving, determining, and assembling steps.

3.   (Currently Amended) A method for assembling nucleic acid sequences comprising the steps of:

providing a plurality of nucleic acid base sequences;

entering identification information [[about]] of each of [[a]] the plurality of nucleic acid base sequences and a respective fixed-length partial sequence located in a terminal region of each of the nucleic acid base sequence s into a table, both of which are associated with each other;

constructing a first consensus sequence based on a first nucleic acid base sequence of the plurality of nucleic acid base sequences;

searching for a second nucleic acid base sequence among remaining ones of the plurality of nucleic acid base sequences which has a second fixed-length partial sequence exactly matching with a [[part]] first partial sequence of said first consensus sequence with reference to said table;

comparing a sequence adjacent to said second fixed-length partial sequence of the second nucleic acid base sequence searched in said searching step with a sequence adjacent to said first fixed-length partial sequence of said first consensus sequence to be sufficiently similar via a greedy alignment algorithm [[, and]] thereby determining whether the searched second nucleic acid base sequence can be assembled to said first consensus sequence or not; and

assembling said second nucleic acid base sequence to said first consensus sequence so as to reconstruct a **reconstructed** first consensus sequence if said step determines that the second nucleic acid base sequence can is determined to be assembled to the first consensus sequence.

4.   (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, wherein a sequence whose base length is the longest among unprocessed the plurality of nucleic acid base sequences is selected as said first nucleic acid base

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sequence.

5.   (Currently Amended) A method for assembling nucleic acid base sequences comprising:

a first step of sorting a plurality of nucleic acid base sequences in descending order of ~~their~~ sequence lengths;

a second step of entering identification information [[about]] of each of the plurality of nucleic acid base sequences and a <u>respective pair of</u> fixed-length partial sequences located in ~~the head end and tail end regions~~ <u>a terminal region thereof</u> ~~input nucleic acid base sequences~~ into a table~~, both of which are associated with each other~~;

a third step of selecting one of the nucleic acid base sequences whose sequence length is the longest among the plurality of ~~unprocessed~~ nucleic acid base sequences~~, and constructing~~ <u>as</u> a first consensus sequence;

a fourth step of moving a fixed length window along said <u>first</u> consensus sequence <u>to define a first fixed-length partial sequence</u> and simultaneously searching for ~~an unprocessed~~ <u>a second</u> nucleic acid base sequence <u>among remaining ones of the plurality of nucleic acid base sequences</u> which has a <u>second fixed-length</u> partial sequence <u>exactly</u> matching with [[a]] <u>the first fixed-length partial</u> sequence defined by said fixed length window with reference to said table;

a fifth step of comparing <u>a sequence adjacent to said first fixed-length partial sequence of</u> said <u>first</u> consensus sequence with <u>a sequence adjacent to said second fixed-length partial sequence of</u> the ~~unprocessed~~ <u>second</u> nucleic acid base sequence searched in said fourth step <u>to be sufficiently similar via a greedy alignment algorithm</u> [[, and]] <u>thereby</u> determining ~~whether~~ <u>said first consensus sequence</u> and the ~~both sequences~~ <u>second nucleic acid base sequence to</u> ~~can~~ be assembled ~~or not~~; and

a sixth step of assembling the <u>second</u> nucleic acid base sequence searched in said fourth step to said <u>first</u> consensus sequence so as to reconstruct a **reconstructed** first consensus sequence if said fifth step determines that the ~~both~~ sequences ~~can~~ <u>are to</u> be assembled,

wherein the fourth step to the sixth step are repeated until said fixed length window completes the scanning throughout said **reconstructed** <u>first</u> consensus sequence, and said third step to said sixth step are repeated ~~if any unprocessed~~ <u>until all of the plurality of</u> nucleic acid base sequence<u>s are selected in the fourth step and compared in</u>

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the fifth step ~~still remains~~.

6.   (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, further comprising a step of specifying a number of said ~~fixed base~~ fixed-length ~~of~~ partial sequences to be entered into said table for ~~one~~ each of the plurality of nucleic acid base sequence_s.

7.   (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, further comprising a step of designating a range of the terminal region ~~head end and tail end regions~~ of said first nucleic acid base sequence from which said fixed-length partial sequences to be entered into said table is extracted.

8.   (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, wherein a base length of said ~~fixed base~~ fixed-length ~~of~~ partial sequence_s to be entered into said table is between ~~at least~~ 10 bases ~~or more~~ and 32 bases ~~or less~~.

9.   (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, further comprising:

a step of specifying an upper limit c ~~on the~~ as an expected ~~value of the~~ number of entries ~~which are detected upon once making reference to~~ retrieved from said table of an identical fixed-length partial sequence located in different nucleic acid base sequences or different positions in the nucleic acid base ~~and their associated input~~ sequences ~~are determined not to be able~~ to be assembled to said first consensus sequences, and

a step of specifying [[the]] a length s of fixed-length partial sequences to be entered into said table as an integer satisfying the following expression (1)

$$s \geq \frac{1}{2} \log \frac{KN}{c} \qquad \cdots (1)$$

where N is the number of said plurality of [[input]] nucleic acid base sequences and K is the number of the fixed-length partial sequences selected from each of the plurality of nucleic acid base sequence_s.

10.   (Currently Amended) The method for assembling nucleic acid base sequences according

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to claim 13, wherein a 3'-end region or a 5'-end region of said first nucleic acid base sequence are simultaneously entered into the table to proceed the searching, comparing, and assembling steps ~~two-way lists are used to implement said consensus sequences~~.

11. (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, wherein [[a]] each of said ~~fixed-base~~ fixed-length ~~of~~ partial sequences is represented by a fixed number of computing words which are independent of [[the]] a length of the fixed-length partial sequences.

12. (Currently Amended) The method for assembling nucleic acid base sequences according to claim 3, wherein only entries in said table corresponding to a key, which is the frequency of occurrence of said second fixed-length partial sequence ~~occurs a previously specified number of times or less~~ in said table, are utilized as said second fixed-length partial sequence for searching for said second nucleic acid base sequence.

13. (New) The method for assembling nucleic acid base sequences according to claim 3, wherein a respective pair of fixed-length partial sequences in the 3'-end region and the 5'-end region said first nucleic acid base sequence.

14. (New) The method for assembling nucleic acid base sequences according to claim 9, wherein c satisfies $NK/4^s \leq c$.

15. (New) The method for assembling nucleic acid base sequences according to claim 9, wherein N= 65536, K=2, and s=10.